

# New vouchered and taxonomically verified records of cave-dwelling populations of catfishes of the genus *Rhamdia* (Siluriformes, Heptapteridae) from Costa Rica

Jairo Arroyave<sup>1</sup>, Arturo Angulo<sup>2,3</sup>, Sonia Gabriela Hernández-Ávila<sup>1</sup>,  
Martín Alonso Buenavad-González<sup>1</sup>, Pablo Rojas-Rodríguez<sup>2</sup>,  
Stanimira Deleva<sup>4,5</sup>, Andrés Ulloa<sup>6,7</sup>, Sophie Picq<sup>8</sup>, Caleb D. McMahan<sup>8</sup>

**1** Instituto de Biología, Universidad Nacional Autónoma de México, Colección Nacional de Peces, Pabellón Nacional de la Biodiversidad, Cto. Centro Cultural, C.U., Coyoacán, 04510 Ciudad de México, Mexico  
**2** Escuela de Biología, Museo de Zoología/Centro de Investigación en Biodiversidad y Ecología Tropical (CIBET) and Centro de Investigación en Ciencias del Mar y Limnología (CIMAR), Universidad de Costa Rica, San Pedro de Montes de Oca, 11501-2060 San José, Costa Rica  
**3** ICTioCR, San Pedro de Montes de Oca, 11501-2060 San José, Costa Rica  
**4** Sede del Sur, Universidad de Costa Rica, 4000 Alamedas, Golfito 60701, San José, Costa Rica  
**5** National Museum of Natural History - Bulgarian Academy of Sciences, 1 Tsar Osvoboditel str., Sofia 1000, Bulgaria  
**6** Centro de Investigación en Ciencias Geológicas, Universidad de Costa Rica, San Pedro de Montes de Oca, 11501-2060 San José, Costa Rica  
**7** Escuela Centroamericana de Geología, Universidad de Costa Rica, San Pedro de Montes de Oca, 11501-2060 San José, Costa Rica  
**8** Field Museum of Natural History, Chicago, Illinois, 60605, USA

Corresponding author: Jairo Arroyave ([jarroyave@ib.unam.mx](mailto:jarroyave@ib.unam.mx))

Academic editor: Maria Elina Bichuette | Received 13 August 2024 | Accepted 15 October 2024 | Published 13 November 2024

<https://zoobank.org/73BF3D41-7039-4A3A-B0BF-E1179F635685>

**Citation:** Arroyave J, Angulo A, Hernández-Ávila SG, Buenavad-González MA, Rojas-Rodríguez P, Deleva S, Ulloa A, Picq S, McMahan CD (2024) New vouchered and taxonomically verified records of cave-dwelling populations of catfishes of the genus *Rhamdia* (Siluriformes, Heptapteridae) from Costa Rica. Subterranean Biology 50: 29–52. <https://doi.org/10.3897/subtbiol.50.134387>

## Abstract

Dedicated ichthyological surveys in two karstic caves in Costa Rica resulted in the discovery of hypogean populations from three epigean species of catfishes of the genus *Rhamdia*. The taxonomic identity of these populations was initially determined based on morphological traits and subsequently corroborated with comparative DNA sequence data in a phylogenetic framework. Individuals from all hypogean populations documented herein exhibit only partial troglomorphy, characterized by only moderate (vs. complete) integumentary depigmentation without extreme eye reduction/loss. A similar pattern of incomplete troglomorphy at the individual level has been observed in other cave-dwelling species/populations of Middle American *Rhamdia*, and tentatively attributed to gene flow with and/or incipient

speciation from epigean lineages. Since most hypogean forms of *Rhamdia* derive from/are part of a larger clade of primarily *R. laticauda*, our discovery of cave-dwelling populations assignable to *R. nicaraguensis* and *R. guatemalensis* is noteworthy, particularly in the case of the former, which represents the first taxonomically verified record of a cave-dwelling population of this epigean species. Among our findings is the remarkable discovery of hypogean populations from two different species of *Rhamdia* (*R. laticauda* and *R. nicaraguensis*) inhabiting the same cave (Gabinarraca). This finding is particularly significant because it represents the first time that cave-dwelling populations from different species of *Rhamdia* are reported to be living in syntopy. Continued discovery of cave-dwelling populations during targeted ichthyological surveys reinforces the notion that our understanding of the diversity of hypogean *Rhamdia* is incomplete and that sustained exploration and taxonomically sound documentation work are paramount to advancing knowledge about the diversity and evolution of these group of Neotropical catfishes.

### Keywords

Cavefishes, hypogean, stygobionts, stygofauna, troglomorphism

## Introduction

With 27 currently valid species distributed throughout most of the tropical Americas, catfishes of the genus *Rhamdia* Bleeker 1858 are a group of moderately diverse Neotropical freshwater fishes noteworthy, among other things, because of their tendency to colonize subterranean waters and maintain resident hypogean populations (Hubbs 1938; Silfvergrip 1996; Perdices et al. 2002; Bichuette and Trajano 2005; Hernández et al. 2015; Arroyave and De La Cruz Fernández 2021a, 2021b; Buenavad-González et al. 2023; Fricke et al. 2024). In fact, several hypogean populations of *Rhamdia* have been described as distinct species, recognized as different from each other and from any of their epigean counterparts (Miller 1984; Wilkens 1993; Weber and Wilkens 1998; Weber et al. 2003; DoNascimento et al. 2004; Bichuette and Trajano 2005), although recent research has called into question the taxonomic validity of some of these cave-adapted species (Arroyave and De La Cruz Fernández 2021b).

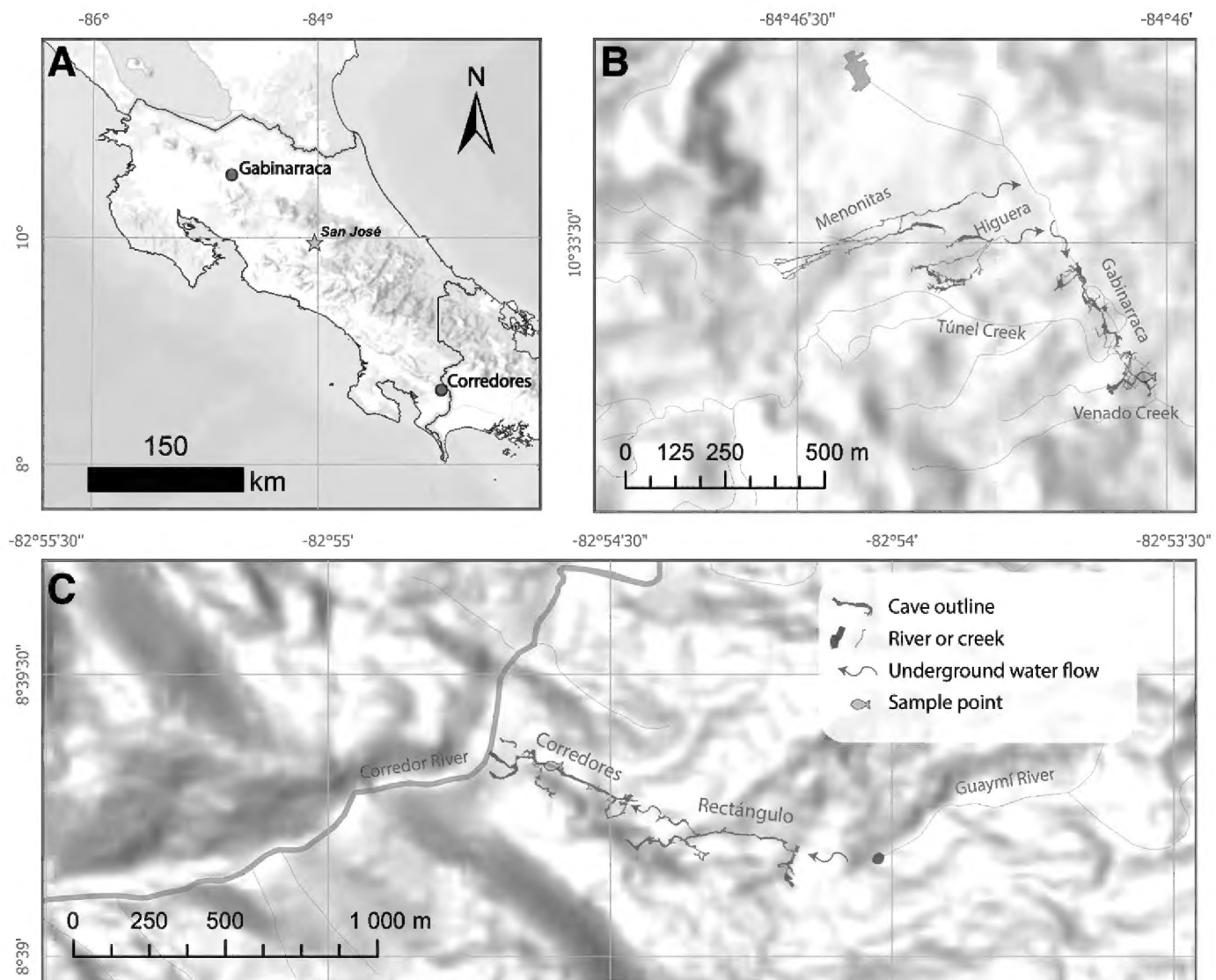
Despite its widespread distribution, the bulk of the subterranean diversity of the genus *Rhamdia* has been primarily described from karstic regions in Mexico. Mexican cave *Rhamdia* includes four of the six currently valid troglobitic species in the genus plus at least 10 cave-dwelling populations taxonomically assigned, for the most part, to the epigean species *R. laticauda* (Kner 1858) (Arroyave and De La Cruz Fernández 2021a, 2021b, Buenavad-González et al. 2023). Recent efforts dedicated to investigating the taxonomic diversity and evolution of Middle American species of *Rhamdia* have shown that the existence of cave-dwelling populations is more geographically widespread than previously thought and that exploration and dedicated ichthyological surveys of underground karstic caves and their associated aquatic environments is likely to result in the discovery of novel subterranean populations, further supporting the idea that cave colonization in the group is widespread (Arroyave and De La Cruz Fernández 2021a, Buenavad-González et al. 2023). Discovery and documentation of novel hypogean populations not only entails the un-

covering of new biodiversity, but also brings forth additional comparative material for future research on the systematics and biogeography of the genus *Rhamdia*. This material (specimens and tissue samples) is key to shed light on the evolution of cave colonization and troglomorphy, intriguing topics that can be studied from both morphological and genetic perspectives.

Whereas recent studies have uncovered and documented the existence of previously unknown cave-dwelling populations of *Rhamdia* in Mexico (Arroyave and De La Cruz Fernández 2021a, Buenavad-González et al. 2023), similar efforts appear to be lacking for the remainder of the distribution of the genus. Costa Rica, a small yet megadiverse country in southern Central America (Avalos 2018), is a part of a natural bridge between North and South America and home to three epigean species of *Rhamdia*: *R. guatemalensis* (Günther 1864), *R. laticauda*, and *R. nicaraguensis* (Günther 1864) (Fricke et al. 2024). Despite harboring several species of *Rhamdia* and having over 250 documented caves (Ulloa et al. 2011), accounts of cave-dwelling populations of *Rhamdia* from Costa Rica are rare, mostly reported by speleologists and mainly supported by anecdotal evidence (Strinati et al. 1987; Debeljak 1988; Juberthie and Strinati 1994; Sandí 2012; Deleva et al. 2023), sometimes including photographs, but never taxonomically verified voucher specimens catalogued in ichthyological collections. Lack of vouchered evidence when documenting hypogean fish fauna—and all biodiversity for that matter—is less than ideal because accurate taxonomic identifications often rely on the direct, close, and careful examination of morphological traits (Rocha et al. 2014; Ceríaco et al. 2016; Nachman et al. 2023). In the case of populations potentially representing undescribed species, the need of voucher specimens is even more pressing. Furthermore, vouchers, when tissue prior to formalin fixation, allow for further taxonomic verification using molecular data, which can also be used in a comparative framework to investigate an assortment of evolutionary questions that require genetic markers.

Historical accounts of hypogean *Rhamdia* from Costa Rica include reported sightings of cave-dwelling forms of *R. guatemalensis* (five sites), *R. nicaraguensis* (one site), and *Rhamdia* sp. (four sites) (Deleva et al. 2023). None of these, however, constitute taxonomically authoritative/verified records (i.e., supported by voucher specimens—not just observations—from which morphology- and/or DNA-based taxonomic identifications have been conducted), thus rendering them potentially unreliable (Rocha et al. 2014; Ceríaco et al. 2016; Nachman et al. 2023). These reports, nonetheless, offer an important baseline to plan and conduct targeted ichthyological surveys aimed at determining the existence and taxonomic identity of any residing cavefish populations.

In a first effort towards properly and accurately documenting the taxonomic diversity of cave *Rhamdia* in Costa Rica, we conducted dedicated ichthyological surveys in two karstic caves with anecdotal reports on the presence of these catfishes: Corredores and Gabinarraca (or Cavernas de Venado) (Fig. 1). This study presents our findings, focusing on the taxonomic nature and phylogenetic placement of these populations, as inferred from morphological and molecular comparative data.

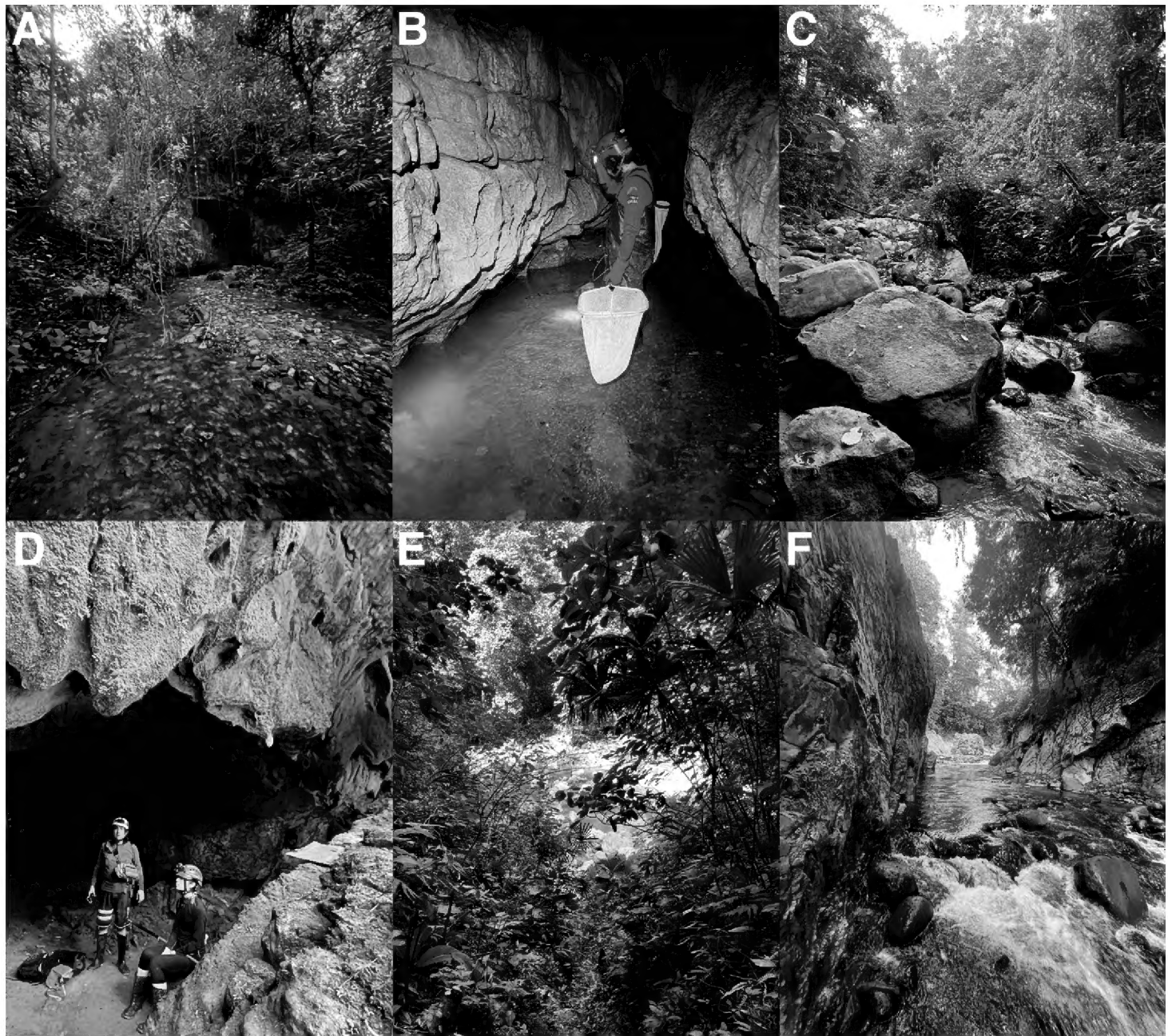


**Figure 1.** Location of the surveyed caves **A** map of Costa Rica displaying the location of Gabinarraca and Corredores caves (green dots) at the country-level scale (borders with Nicaragua to the north and Panama to the south highlighted in light purple). Maps displaying the location of the surveyed caves at the local scale, including geomorphological and hydrological features: **B** Gabinarraca and **C** Corredores.

## Methods

### Area of study

Gabinarraca and Corredores caves are located in the Costa Rican provinces of Alajuela and Puntarenas, respectively (Fig. 1A). Each cave constitutes the terminal segment of a karst system comprised of multiple interconnected caves with a perennial underground river (Fig. 1B, C). Gabinarraca cave is on the Caribbean versant of northwestern Costa Rica (although very near the continental water divide), c. 11 km northwest of the Arenal volcano. It is part of the Venado karstic system, which developed from Miocene limestone from the Venado Formation, and comprises three main caves: Menonitas (1620 m in length), Higuera (954 m in length), and Gabinarraca (2351 m in length), totaling almost 5 km of underground passages (Ulloa et al. 2021) (Fig. 1B). Not only is Gabinarraca cave the longest of the Venado karstic system caves, but it is also the best known, since it has been a tourist attraction for over two decades (Ulloa et al. 2021) (Fig. 2A, B). Corredores cave, on the other hand, is located on the Pacific versant of southern Costa Rica, very close to the border with Panama, c. 3.5 km east of Ciudad Neily (Fig. 1A). It is part of the Cerro Corredores karst system, which extends over a



**Figure 2.** Photographs displaying physical features of the surveyed caves and associated rivers/streams **A** Gabinarraca cave entrance, showing the outflow of water into Quebrada El Túnel **B** inside Gabinarraca cave while electrofishing **C** Quebrada El Túnel close to the entrance of Gabinarraca cave **D** Corredores cave entrance **E** Río Corredor as seen from the cave entrance higher up **F** Río Corredor riverbed at a small canyon on the way to the cave access point.

length of c. 3 km carrying water from the Guaymí River that infiltrates from the east through a sinkhole and flows underground northwest through several caves, including La Bruja (221 m), El Rectángulo (1411 m), and Corredores (1624 m), before emerging from the aquifer and flowing into the Corredor River (Peacock and Hempel 1993) (Figs 1C, 2D–F). The karst in the area develops in Eocene limestones associated with the Fila de Cal Formation (Chesnel and Rodríguez 2021).

### Specimen sampling and preservation

Both sampled caves are wet (containing active watercourses but not fully flooded or submerged) and mostly horizontal, and therefore did not require specialized vertical caving techniques for surveying and sampling. Specimen sampling was accomplished using a combination of baited minnow traps and electrofishing. Inside the surveyed

The map displays the topography of the study area, with the Continental water divide running diagonally across the center. Major rivers shown include Rio Naranjo, Rio Corobio, Rio Pasate, Rio Rio, and Rio Parase. Key locations marked include Bijagua, Buenavista, San Jorge, Cote, Venado, Monterrey, La Fortuna, Tilarán, Santa Rosa, Tzuc, and Canas. Sampling points 1 through 6 are indicated by black dots. The map also shows the locations of Parque Nacional Volcán Tenorio and Parque Nacional Volcán Arenal. A scale bar indicates distances up to 10 km, and a north arrow is present in the upper right corner. Coordinates are provided along the bottom and right edges.

**Figure 3.** Collecting sites of epigeal populations of *Rhamdia* sampled in this study **1** Quebrada El Túnel (at Gabinarraca cave entrance) **2** Quebrada El Túnel (further downstream from Gabinarraca cave entrance) **3** Río Pataste **4** Río Arenal **5** Quebrada Palma, and **6** Quebrada Altamira. All sites are within the Alajuela province, Atlantic versant. Black outline in map corresponds to the continental water divide.

**Table 1.** Sampling localities with their respective species, catalog/vouchers numbers, and GenBank accession numbers of sequences generated in this study and used in phylogenetic analyses. \*at Gabinarraca cave entrance; \*\*further downstream from Gabinarraca cave entrance.

Habitat	Locality	Coordinates	Municipality	Province	Basin	Versant	Species	Catalog (n)	Tissued vouchers	DNA voucher	GenBank Accession				
Hypogean	Gabinarraca cave	10°33'17"N, 84°46'01"W	Venado	Alajuela	Río Frío	Atlantic	<i>Rhamdia laticauda</i>	UCR 3323-01 (6)	JA1913-17	JA1913	PQ451515	PQ458956			
										JA1914	PQ451516	PQ458957			
										JA1915	PQ451517	PQ458958			
										JA1916	PQ451492	PQ458959			
								<i>Rhamdia nicaraguensis</i>	UCR 3323-02 (13)	JA1902-12	JA1902	PQ451502	PQ458966		
											JA1903	n/a	PQ458967		
											JA1904	PQ451503	PQ458968		
											JA1905	PQ451504	PQ458969		
											JA1906	PQ451505	PQ458970		
											JA1907	PQ451506	PQ458971		
											JA1908	PQ451507	PQ458972		
											JA1909	PQ451508	PQ458973		
Epigean	Corredores cave	08°39'23"N, 82°54'44"W	Ciudad Neily	Puntarenas	Río Coto	Pacific	<i>Rhamdia guatemalensis</i>	UCR 3330-01 (8)	JA2068-74	JA2068	PQ451499	PQ458950			
										JA2070	n/a	PQ458951			
										JA2071	PQ451500	PQ458952			
										JA2072	PQ451501	PQ458953			
								<i>Rhamdia nicaraguensis</i>	UCR 3324-02 (3)	JA2073	n/a	PQ458954			
											JA2074	n/a	n/a		
										UCR 3324-01 (3)	JA1921-23	JA1921	PQ451518	PQ458960	
												JA1922	PQ451493	PQ458961	
												JA1923	PQ451519	PQ458962	
												JA1918	PQ451511	PQ458977	
										<i>Rhamdia nicaraguensis</i>	UCR 3324-02 (3)	JA1918-20	JA1919	PQ451512	PQ458978
													JA1920	PQ451513	PQ458979
Epigean	Quebrada El Túnel**	10°33'17"N, 84°45'20"W	Venado	Alajuela	Río Frío	Atlantic	<i>Rhamdia laticauda</i>	UCR 3325-01 (7)	JA1924-30			JA1927	PQ451520	n/a	
												JA1928	PQ451494	PQ458963	
										n/a	n/a	n/a			
										n/a	n/a	n/a			

Habitat	Locality	Coordinates	Municipality	Province	Basin	Versant	Species	Catalog (n)	Tissued vouchers	DNA	GenBank Accession	
										voucher	COI	CYB
Epigeal	Río Arenal	10°30'09"N, 84°35'38"W	Venado	Alajuela	Río San Carlos	Atlantic	<i>Rhamdia laticauda</i>	UCR 3326-01 (8)	JA1952-59	JA1955	PQ451495	PQ458964
							<i>Rhamdia nicaraguensis</i>	UCR 3326-02 (2)	JA1960-61	n/a	n/a	n/a
	Río Patate	10°34'07"N, 84°40'02"W	Venado	Alajuela	Río Frío	Atlantic	<i>Rhamdia laticauda</i>	UCR 3327-01 (4)	JA1943-46	JA1946	PQ451521	n/a
							<i>Rhamdia nicaraguensis</i>	UCR 3327-02 (7)	JA1936-42	JA1939	n/a	PQ451514
	Quebrada Altamira	10°44'01"N, 85°03'34"W	Bijagua	Alajuela	Río Zapote	Atlantic	<i>Rhamdia laticauda</i>	UCR 3328-01 (15)	JA1804-11	JA1804	PQ451496	PQ458955
							<i>Rhamdia laticauda</i>	UCR 3329-01 (5)	JA1734-38	JA1734	PQ451498	PQ458965
	Quebrada Palma	10°29'54"N, 84°41'19"W	Palma	Alajuela	Río San Carlos	Atlantic	<i>Rhamdia nicaraguensis</i>	UCR 3329-02 (5)	JA1729-33	n/a	n/a	n/a
							<i>Rhamdia laticauda</i>	UCR 3329-02 (5)	JA1729-33	n/a	n/a	n/a

## Comparative data generation and analysis

To document patterns of phenotypic and genetic variation, and to shed light on the taxonomic nature of the cave-dwelling populations of *Rhamdia* reported herein, we generated meristic and morphometric data from hypogean samples as well as DNA sequence data from both hypogean and epigean samples. Morphometric measurements and meristic counts follow previous taxonomic studies of *Rhamdia* (Silfvergrip 1996; Hernández et al. 2015; Buenavad-González et al. 2023). All measurements were taken on the left side of specimens using a Mitutoyo digital caliper (precision = 0.1 mm; accuracy =  $\pm 0.02$  mm). Comparative genetic data consisted of partial fragments of the mitochondrial protein-coding genes cytochrome c oxidase subunit I (COI) and cytochrome b (CYTB). We generated COI and CYTB data from representatives of all cave-dwelling populations documented herein, as well as from samples of epigean *Rhamdia* collected during the fieldwork component of this study and relevant for comparative purposes (Table 1). To increase our precision in estimating the phylogenetic placement of the Costa Rican cave-dwelling populations with respect to the entire Middle American clade of the genus, we broadened the taxonomic and geographic coverage of samples used for phylogenetic analyses by including additional COI and CYTB sequences of *Rhamdia* retrieved from GenBank ([www.ncbi.nlm.nih.gov/Genbank](http://www.ncbi.nlm.nih.gov/Genbank)) and from unpublished data previously generated by the lead author (JA). To generate DNA sequence data, we first extracted total genomic DNA from fresh tissue samples using the Qiagen DNeasy Tissue Extraction Kit, following the manufacturer's protocol. We amplified and sequenced COI and CYTB following the procedures (primers and PCR thermal profiles) employed in recent molecular phylogenetic studies of the genus that used the same markers (Arroyave and De La Cruz Fernández 2021a, 2021b, Buenavad-González et al. 2023). DNA extraction, amplification, and sequencing were carried out at Laboratorio de Secuenciación Genómica de la Biodiversidad y de la Salud (Instituto de Biología, UNAM) and Pritzker Molecular Laboratory at the Field Museum of Natural History (FMNH). Contig assemblage, sequence editing, multiple sequence alignment—using MUSCLE (Edgar, 2004)—and the calculation of uncorrected genetic distances ( $p$ -distances) were performed in Geneious Prime 2024.0.7 (<https://www.geneious.com>). The resulting COI and CYTB matrices consisted of 116 and 126 ingroup (trans-Andean/Middle American *Rhamdia*) terminals, including representatives from 9 and 10 of the 11 valid species in the clade, respectively. In addition to the individual gene alignments, we analyzed a concatenated alignment—assembled with the software 2matrix (Salinas and Little 2014)—taxonomically limited to 59 ingroup terminals (with voucher specimens) from nine species for which both COI and CYTB data were available. In all cases, the cis-Andean species *Rhamdia quelen* was used as the outgroup and root, based on previous phylogenetic research that supports the reciprocal monophyly between cis- and trans-Andean clades of *Rhamdia* (Perdices et al. 2002; Hernández et al. 2015; Arroyave and De La Cruz Fernández 2021b). For each alignment, statistical selection of the best-fit model of nucleotide substitution was implemented with the software jModelTest2 (v. 2.1.10) (Darriba et al. 2012) under the following likelihood settings:

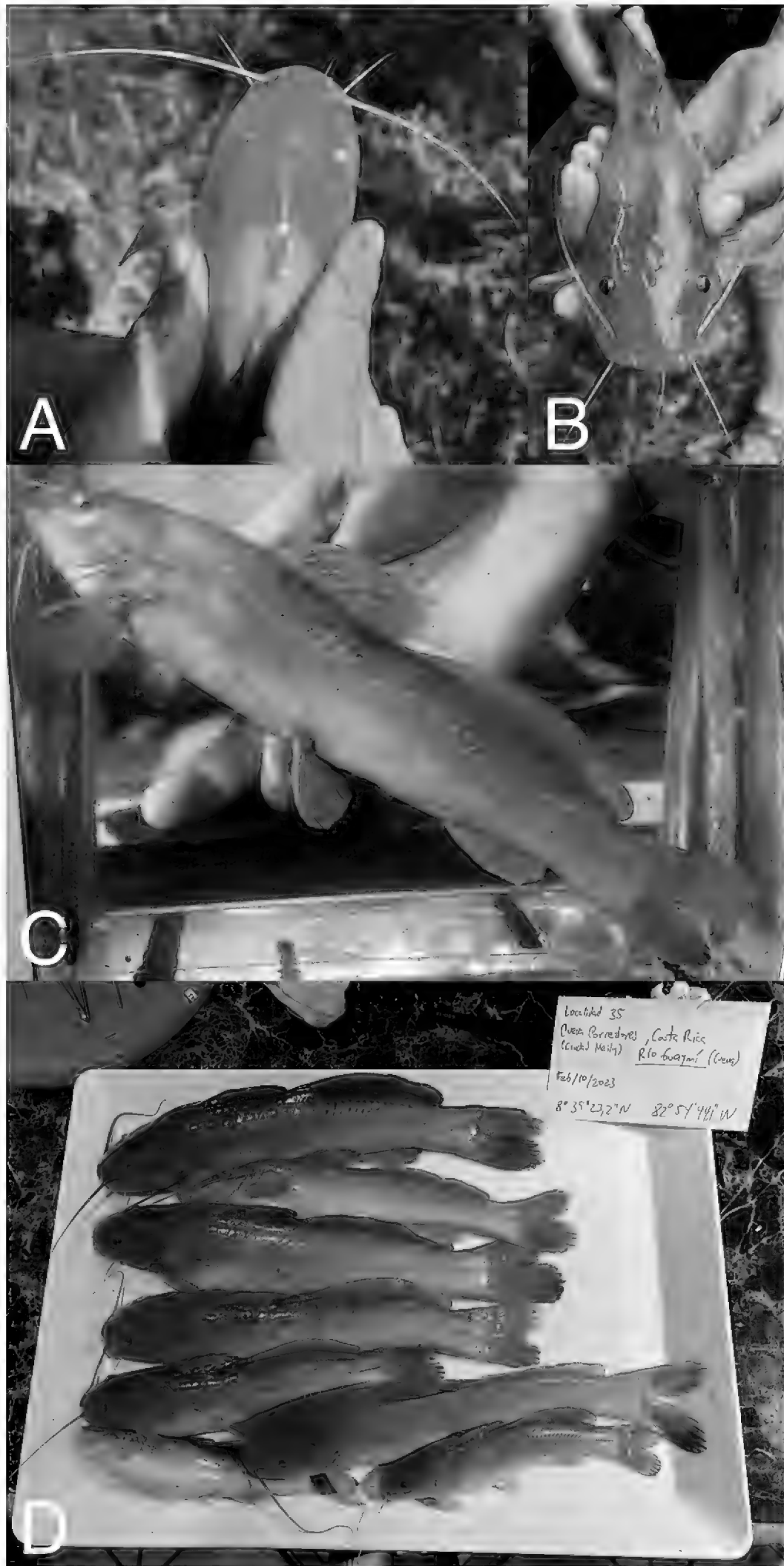
number of substitution schemes = 3; base frequencies = +F; rate variation = +I and +G with nCat = 4; base tree for likelihood calculations = ML optimized; and base tree search = NNI, effectively evaluating 24 alternative models. We inferred a phylogenetic tree for each individual gene matrix as well as for the concatenated alignment using the software RAxML-NG (v. 1.2.1) (Kozlov et al. 2019) under their respective best-fit models of molecular evolution. Clade support was estimated using the bootstrap character resampling method (Felsenstein 1981) based on 1000 pseudoreplicates.

## Results

Our sampling efforts in the surveyed caves (Corredores and Gabinarraca) resulted in the discovery of three cave-dwelling populations of *Rhamdia*, identified as members of the species *R. guatemalensis* (Corredores cave; n = 8) (Figs 4, 7), *R. laticauda* (Gabinarraca cave; n = 6) (Figs 5, 7), and *R. nicaraguensis* (Gabinarraca cave; n = 13) (Figs 6, 7). Furthermore, we collected individuals from epigean populations of both *R. laticauda* and *R. nicaraguensis*, from six and five localities, respectively (Table 1). Taxonomic identifications were initially based on external morphology and further corroborated by comparative molecular data in a phylogenetic context (Figs 8–10). All hypogean populations displayed partial loss of body pigmentation, resulting in a yellowish coloration in life, which contrasts with the dark, melanic phenotype typical of epigean forms (Fig. 6D). Notably, none of the hypogean populations exhibited a pattern of eye reduction/loss, except for a single specimen of *R. guatemalensis* from the Corredores cave which displayed a slight and asymmetric eye degeneration and reduction (Fig. 4A).

Morphological and meristic data from the specimens collected at the surveyed caves are presented in Tables 2, 3. Inter- and intraspecific variation in morphological traits of taxonomic importance (i.e., those used to distinguish among the three species of *Rhamdia* present in Costa Rica) such as pectoral spine serration, interdorsal space, length of barbels, and head length, conformed with the expectations of our species designations.

GenBank accession numbers corresponding to the DNA sequence data generated in this study (COI and CYTB) are presented in Table 1. Regardless of marker/matrix, the inferred phylogenies (Figs 8–10) unambiguously place the Costa Rican cave-dwelling populations of *Rhamdia* documented herein (colored in red) well nested within the *R. guatemalensis* clade (in the case of samples from the Corredores cave) and the “*R. laticauda*-group” clade (Weber and Wilkens 1998) (in the case of samples from the Gabinarraca cave). Although these phylogenies consistently recover *R. laticauda* deeply paraphyletic, samples from Gabinarraca morphologically identified as *R. laticauda* were resolved within a well-supported clade consisting exclusively of Costa Rican samples of this species, both hypogean and epigean (Figs 8–10). Similarly, samples from Gabinarraca cave identified morphologically as *R. nicaraguensis* nested within a moderately to well-supported clade consisting exclusively of *R. nicaraguensis* samples, including epigean ones. Notably, within the “*R. laticauda*-group” clade, *R. nicaraguensis* was consistently recovered as monophyletic (Figs 8–10).



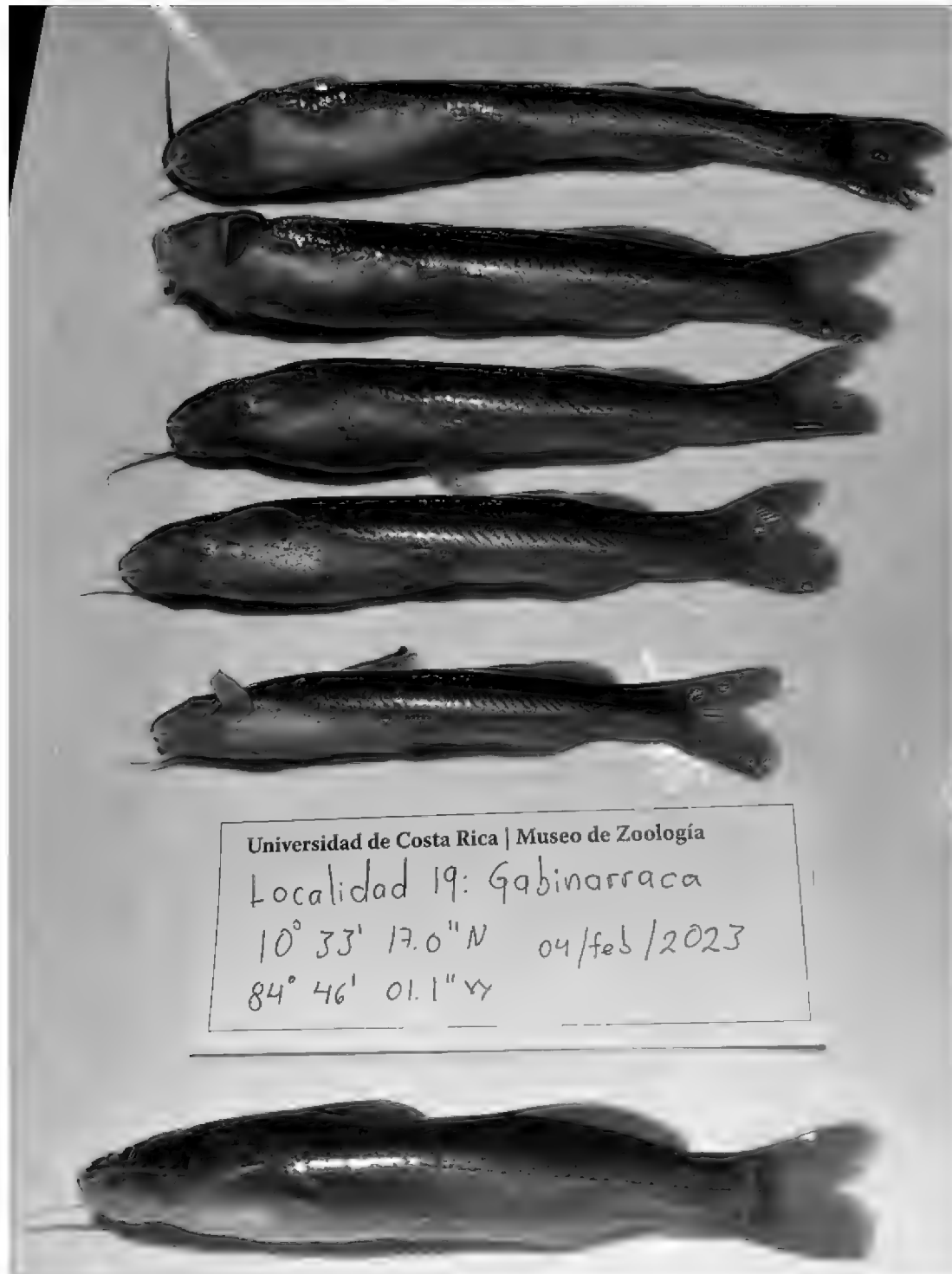
**Figure 4.** Photographs of hypogean *Rhamdia guatemalensis* from Corredores cave **A, B** dorsal views of head and anterior part of body in life after capture **C** lateral view of live specimen in aquarium **D** totality of specimens collected ( $n = 8$ ), immediately postmortem and before tissueing and preservation.

**Table 2.** Meristic comparative data from samples of hypogean populations of *Rhamdia* spp. from Gabinarraca and Corredores caves. Meristic traits abbreviations as follows: PFR = pectoral-fin rays, PvFR = pelvic-fin rays, DFR = dorsal-fin rays, ARF = anal-fin rays, uCFR = upper caudal-fin rays, and lCFR = lower caudal-fin rays. Caudal-fin rays numbers (x,y,z) correspond to unsegmented (x), unbranched segmented (y), and branched segmented (z) rays.

Cave	Species	Catalog	Voucher	PFR	PvFR	DFR	AFR	uCFR	lCFR
Gabinarraca	<i>Rhamdia laticauda</i>	UCR 3323-01	3323-01-A	I-9	6	I-6	9	3,2,8	3,2,9
			JA1906	I-9	7	I-6	9	3,2,9	3,2,9
			JA1902	I-9	7	I-5	10	3,2,9	3,2,8
			3323-01-B	I-9	7	I-6	9	3,2,8	3,2,10
	<i>Rhamdia nicaraguensis</i>	UCR 3323-02	JA1903	I-9	7	I-5	9	3,2,6	3,2,8
			JA1904	I-9	7	I-6	10	3,2,9	3,2,10
			JA1905	I-9	7	I-6	9	3,2,8	3,2,9
			JA1907	I-9	7	I-6	9	3,2,9	3,2,9
			JA1908	I-9	8	I-6	9	3,2,8	3,2,8
			JA1909	I-9	7	I-6	9	3,2,9	3,2,9
			JA1910	I-9	7	I-6	9	3,2,9	3,2,9
			JA1911	I-9	7	I-6	9	3,2,7	3,2,9
			JA1912	I-9	7	I-6	9	3,2,9	3,2,8
Corredores	<i>Rhamdia guatemalensis</i>	UCR 3330-01	3330-01-A	I-7	6	I-6	9	3,2,9	3,2,10
			JA2068	I-8	7	I-6	9	3,2,9	3,2,10
			JA2069	I-9	7	I-6	9	3,2,9	3,2,10
			JA2070	I-9	6	I-6	8	3,2,8	3,2,9
			JA2071	I-8	7	I-6	8	3,2,9	3,2,9
			JA2072	I-7	6	I-7	8	3,2,9	3,2,7
			JA2073	I-9	7	I-6	9	3,2,9	3,2,9
			JA2074	I-9	7	I-6	9	3,2,8	3,2,9

Discussion

In the most recent and comprehensive review of Costa Rican cave-dwelling fauna, Deleva et al. (2023) reported on the presence of hypogean populations of *R. guatemalensis* in the Corredores and Bananal cave systems, as well as in other adjacent caves. Our results confirm the presence of *Rhamdia* catfishes in the Corredores cave (Figs 4, 7–10). The existence of hypogean populations of *R. guatemalensis* in other caves from southern Costa Rica—such as Bananal—has yet to be verified; however, these may seem likely given our Corredores cave findings and previous reports from the region (anecdotal and otherwise). The existence of cave-dwelling populations of *R. guatemalensis* in Costa Rica is noteworthy considering that most hypogean populations of *Rhamdia* that have been documented so far are derivatives of *R. laticauda*, either as cave-adapted populations or as species-level lineages within the “*R. laticauda*-group” clade (Arroyave and De La Cruz Fernández 2021a, 2021b, Buenavad-González et al. 2023). To our knowledge, the Corredores cave population effectively constitutes the fourth taxonomically verified record of a hypogean population of *R. guatemalensis*; the first three being from Mexican caves in the states of Tabasco (Grutas de Coconá) and Chiapas (Los Bordos and El Encanto caves) (Buenavad-González et al. 2023).



**Figure 5.** Photograph of hypogean *Rhamdia laticauda* from Gabinarraca cave. Totality of specimens collected ( $n = 6$ ), immediately postmortem and before tussing and preservation.

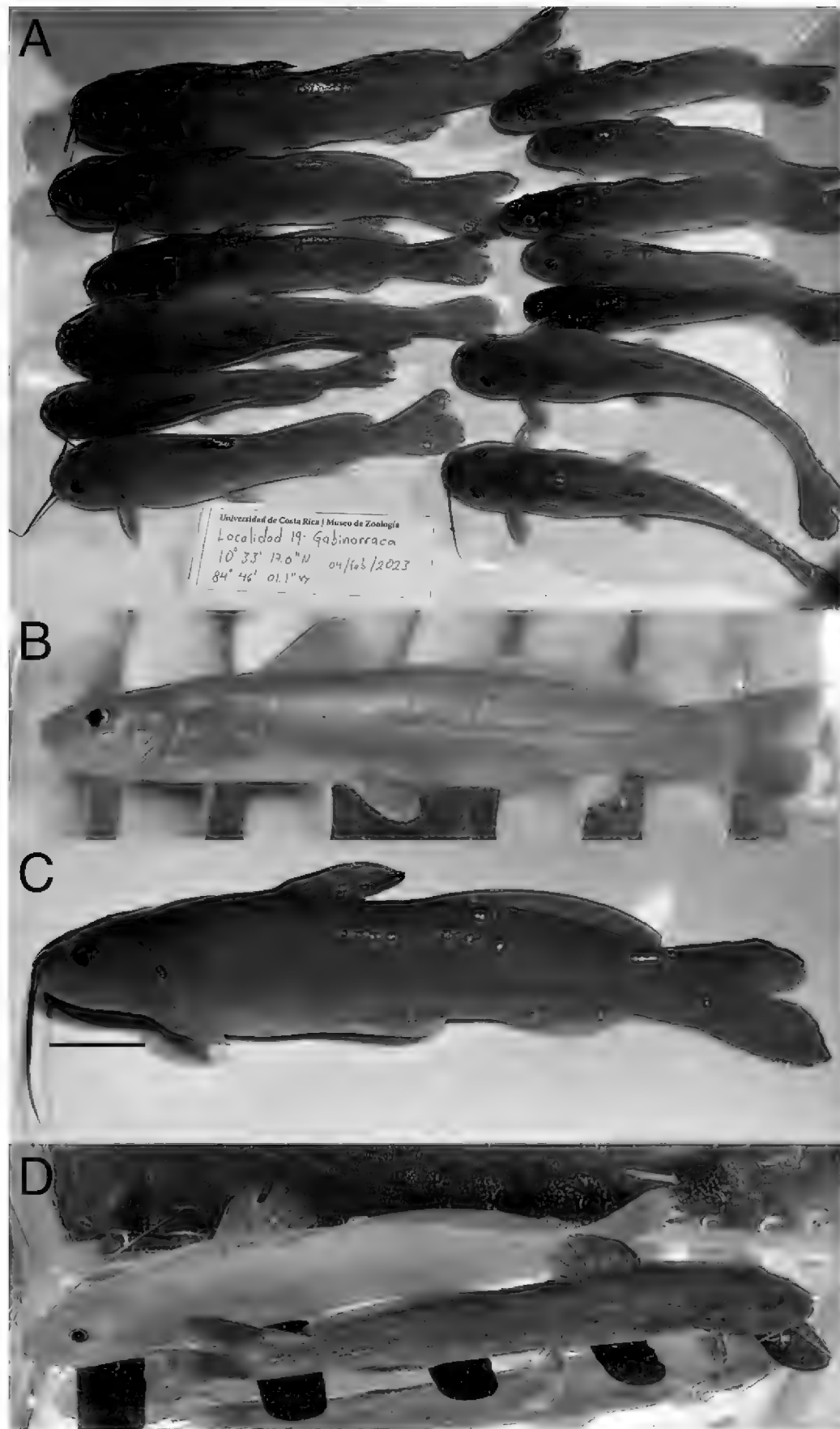
Despite the Corredores cave population not exhibiting full troglomorphism (due to the presence of eyes), it appears to be the most depigmented of all four *R. guatemalensis* hypogean populations documented to date (Fig. 4).

Remarkably, among our findings is the discovery of syntopic hypogean populations from two different *Rhamdia* species (*R. laticauda* and *R. nicaraguensis*) inhabiting the Gabinarraca cave system. This finding is noteworthy because it represents the first taxonomically verified record of a cave-dwelling population of *R. nicaraguensis*. Furthermore, the population of *R. laticauda* from Gabinarraca cave constitutes the latest addition to the extensive list of hypogean records for this epigeal species—which includes five populations from the karstic Sierra de Zongolica in the state of Veracruz (Arroyave and De La Cruz Fernández 2021a) and two populations from karstic caves

**Table 3.** Morphometric comparative data from samples of hypogean populations of *Rhamdia* spp. from Gabinarraca and Corredores caves. Measurements abbreviations as follows: SL = Standard Length, HL = Head Length, BW = Body Width, DFH = Dorsal Fin Height, DSH = Dorsal-fin Spine Height, AFL = Anal Fin Length, AdFL = Adipose Fin Length, PFL = Pectoral Fin Length, PSL = Pectoral-fin Spine Length, PvFL = Pelvic Fin Length, ISL = Interdorsal Space Length, CPL = Caudal Peduncle Length, CPD = Caudal Peduncle Depth, IOW = Interorbital Width, ORB = Orbital Diameter, SNT = Snout Length, MBL = Maxillary Barbel Length, MdBL = Mandibular Barbel Length, MeBL = Mental Barbel Length.

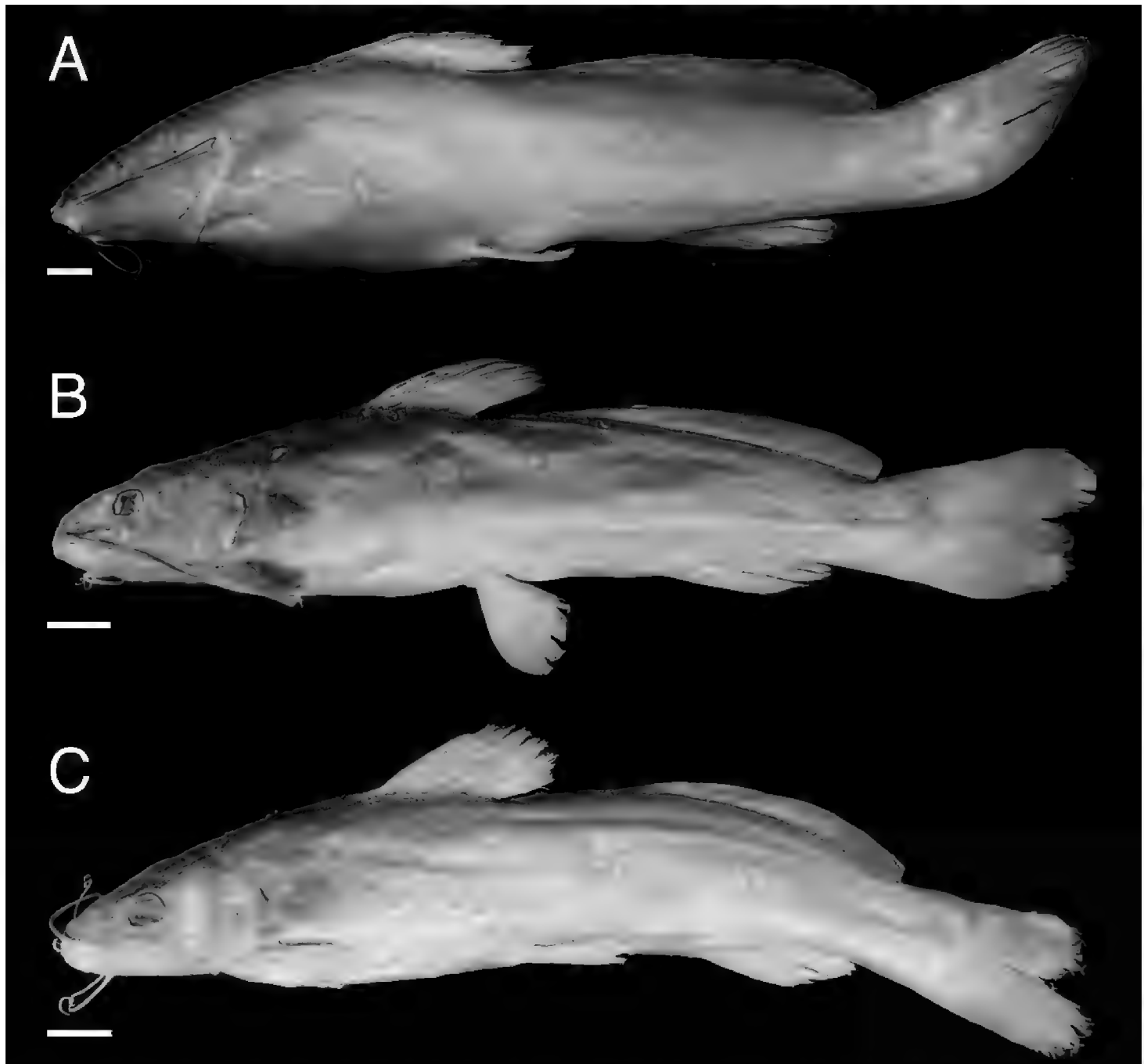
	Gabinarraca Cave						Corredores Cave		
	<i>Rhamdia laticauda</i> (n = 4)			<i>Rhamdia nicaraguensis</i> (n = 9)			<i>Rhamdia guatemalensis</i> (n = 8)		
	Range	Mean	SD	Range	Mean	SD	Range	Mean	SD
mm									
SL	119.94–198.00	150.45	34.85	107.16–171.00	132.82	21.23	124.41–237.00	193.43	45.70
HL	29.75–43.29	34.45	6.04	24.80–40.43	31.32	5.50	28.60–52.92	43.10	10.27
% SL									
HL	21.46–24.99	23.14	1.74	22.64–24.64	23.53	0.67	20.49–22.99	22.30	0.78
BW	16.35–17.92	17.19	0.64	15.48–18.14	16.56	0.76	18.00–18.91	18.48	0.32
DFH	13.25–14.75	14.00	0.64	10.17–14.88	13.34	1.28	12.48–15.64	13.93	1.03
DSH	5.32–6.20	5.81	0.37	4.19–5.05	4.55	0.29	5.98–6.72	6.35	0.28
AFL	17.29–18.80	17.95	0.63	18.32–21.42	20.15	1.05	17.61–19.60	18.59	0.60
AdFL	40.80–42.41	41.93	0.75	39.90–45.58	43.84	1.99	36.54–38.39	37.74	0.57
PFL	10.49–13.89	12.22	1.50	12.45–13.79	13.15	0.45	12.16–13.89	12.95	0.57
PSL	6.67–8.58	7.45	0.89	7.02–8.89	7.88	0.62	7.30–9.24	8.41	0.62
PvFL	9.90–12.61	11.32	1.40	11.43–12.94	12.08	0.47	11.01–13.12	11.63	0.83
ISL	4.61–4.78	4.69	0.08	1.46–2.43	1.67	0.30	5.27–7.75	6.67	0.85
CPL	16.35–18.94	17.47	1.22	17.79–18.96	18.24	0.41	17.90–20.23	18.48	0.75
CPD	9.95–10.35	10.11	0.17	9.78–11.12	10.30	0.40	9.71–11.36	10.83	0.55
% HL									
IOW	36.13–42.67	38.94	2.72	35.02–39.45	37.13	1.46	40.05–46.97	43.71	2.14
ORB	17.39–20.10	18.65	1.23	15.94–20.24	17.98	1.44	9.01–16.09	12.07	2.16
SNT	37.75–41.49	39.48	1.60	35.54–41.75	38.15	1.77	32.72–41.85	36.82	2.73
MBL	100.11–117.27	111.31	7.64	88.97–136.11	121.53	14.67	124.49–228.91	158.01	33.37
MdBL	47.62–54.66	50.70	3.01	54.28–74.97	60.26	5.95	62.72–90.31	72.73	9.92
MeBL	27.66–36.79	32.88	3.97	32.69–46.50	35.71	4.21	41.76–55.44	47.45	5.06

in the state of Chiapas (Buenavad-González et al. 2023)—further supporting the notion that *R. laticauda* is the quintessential cave colonizer species in the genus. Lastly, and perhaps more interestingly, this is the first time that cave-dwelling populations from different species of *Rhamdia* are reported to be living in syntopy. Coexistence of multiple species of hypogean fishes in the same cave is not widespread but neither uncommon; around 40% of obligate cavefish species co-occur with other such species, although very rarely totaling more than two syntopic species per cave (Trajano 2001). Approximately half of the known instances of syntopy in cavefishes involve species relatively distant phylogenetically, while the other half involve species from the same family although mostly from different genera (Niemiller and Soares 2015). Apart from the case of *Rhamdia* in the Gabinarraca cave reported herein, the only other known instances of intrageneric syntopy in cavefishes are restricted to viviparous brotulas of the genus *Lucifuga* Poey 1858 in two Cuban caves, with three and two syntopic species,



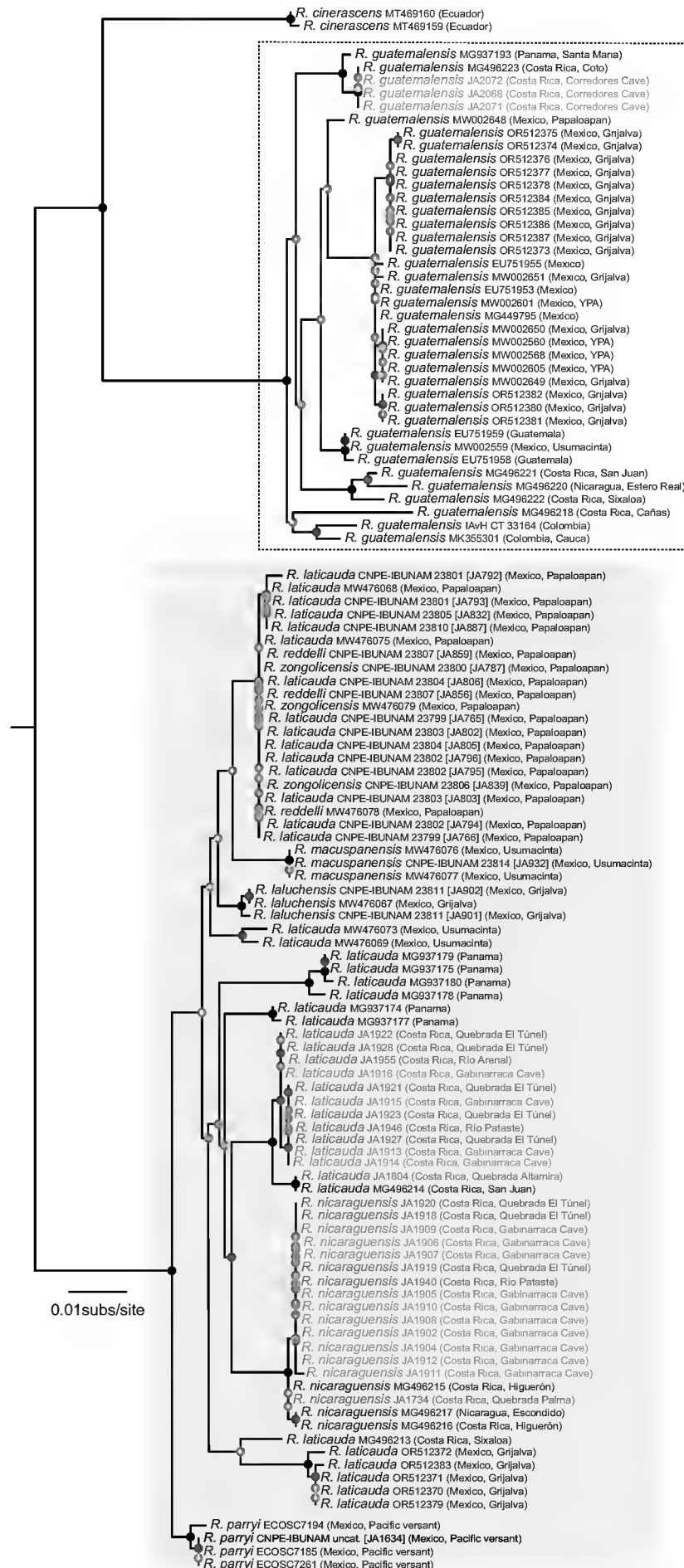
**Figure 6.** Photographs of hypogean *Rhamdia nicaraguensis* from Gabinarraca cave **A** totality of specimens collected ( $n = 13$ ), immediately postmortem and before tissueing and preservation **B** lateral view of live specimen in aquarium **C** lateral view of specimen immediately postmortem. Metacercariae (two) of the parasitic fluke *Clinostomum* sp. are visible at the base of the anal fin **D** live specimens (in aquarium) of hypogean (Gabinarraca, yellow) and epigean (Quebrada El Túnel, dark brown) *R. nicaraguensis*. Scale bar: 1 cm.

respectively (Trajano 2001). It is generally assumed that coexistence in syntopy requires some type of resource (mainly food and space) partitioning so as to minimize competition (Pianka 1973), and this is especially true of closely related and morphologically

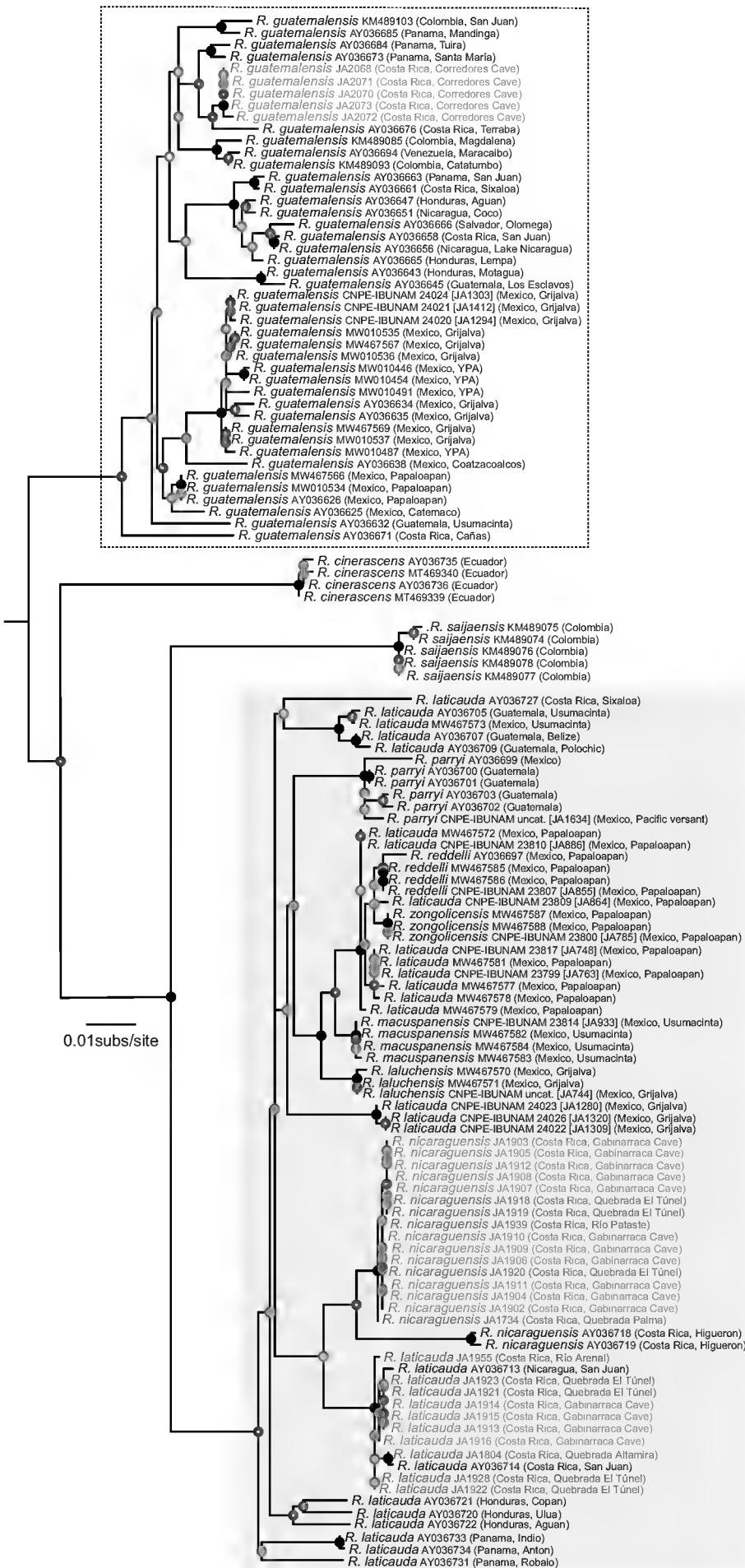


**Figure 7.** Photographs of preserved representatives of the populations of cave-dwelling *Rhamdia* from Costa Rica reported in this study **A** *R. guatemalensis* from Corredores cave (UCR 3330-01; 230 mm TL) **B** *R. nicaraguensis* from Gabinarraca cave (UCR 3323-02; 165 mm TL), and **C** *R. laticauda* from Gabinarraca cave (UCR 3323-01; 158 mm TL). Scale bar: 1 cm.

similar species co-occurring in hypogean habitats that are generally oligotrophic and with simplified food webs (Niemiller and Soares 2015). In some well-documented cases, habitat partitioning and/or differences in diet between syntopic cavefish species have been posited as the evolutionary and ecological mechanisms allowing coexistence with minimum competition (Trajano 2001). This pattern of ecological differentiation and resource partitioning in cavefishes, however, has only been demonstrated in some instances of syntopy involving relatively phylogenetically distant species (from different genera and families). In cases of closely related and morphologically conserved syntopic cavefish species such as *Lucifuga* spp. from Cuban caves, the mechanisms enabling local coexistence are not fully understood, although it appears that competitive-driven shifts in diet and habitat preferences have yet to evolve (Trajano 2001). With hypogean populations of two species of *Rhamdia* (*R. laticauda* and *R. nicaraguensis*)



**Figure 8.** Phylogenetic relationships of Middle American *Rhamdia* inferred from comparative COI data. Colored circles on nodes indicate degree of clade support as determined by bootstrap values: black > 95, 95 ≥ blue ≥ 75, red < 75. Terminal names as follow: Species name + GenBank accession or catalog/voucher (for new/unpublished sequences) + country, basin (in parenthesis). Terminals corresponding to samples from populations of Costa Rican hypogean *Rhamdia* (documented herein) in red. Terminals corresponding to samples from Costa Rican epigean *Rhamdia* collected in this study in blue. Outgroup taxon (*Rhamdia quelen*) not shown. The dashed rectangle indicates the *R. guatemalensis* clade, whereas the light gray rectangle indicates the “*R. laticauda*-group” clade, inclusive of *R. nicaraguensis*, *R. parryi*, and the four Mexican stygobitic species.



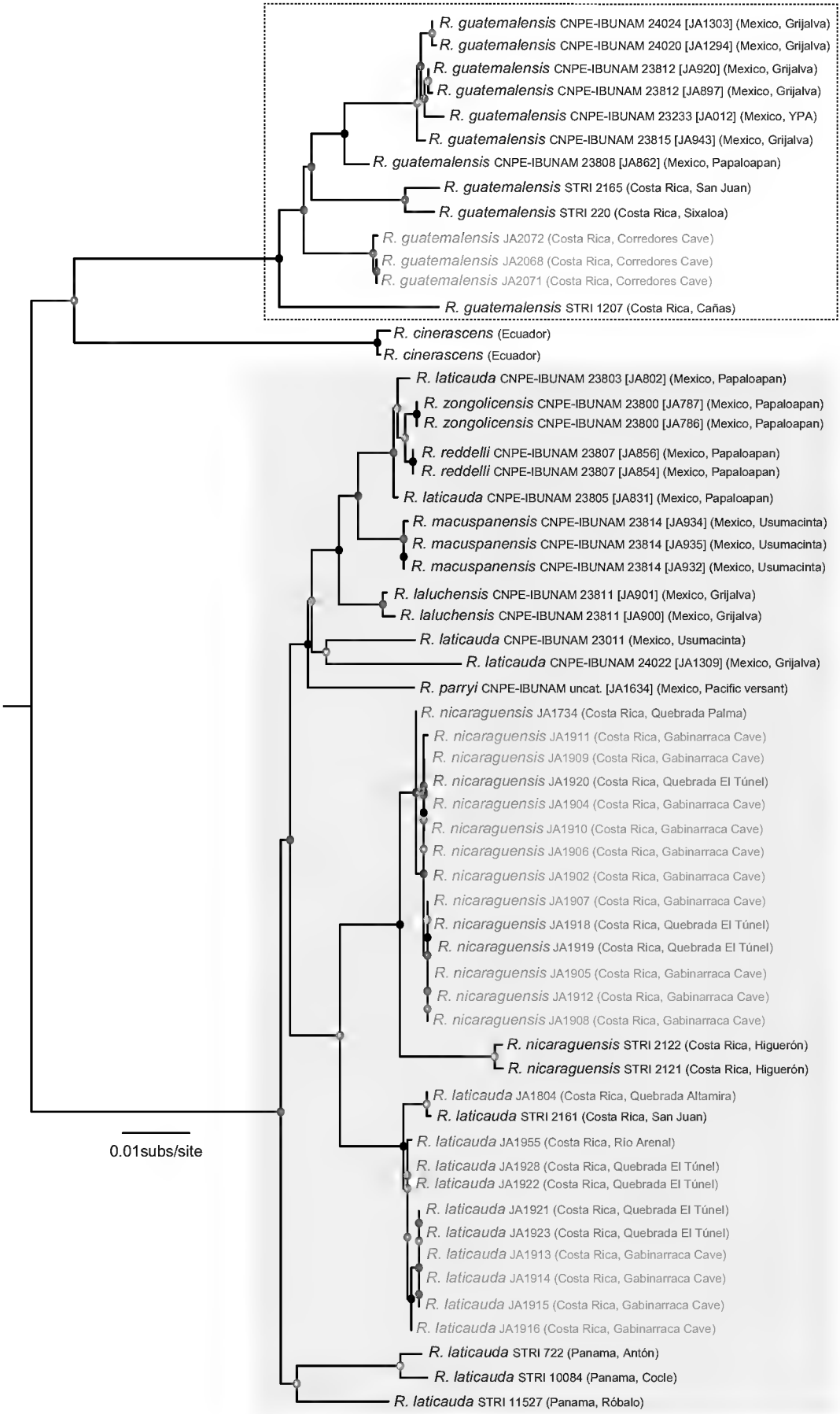
**Figure 9.** Phylogenetic relationships of Middle American *Rhamdia* inferred from comparative CYTB data. Colored circles on nodes indicate degree of clade support as determined by bootstrap values: black > 95, 95 ≥ blue ≥ 75, red < 75. Terminal names as follow: Species name + GenBank accession or catalog/voucher (for new/unpublished sequences) + country, basin (in parenthesis). Terminals corresponding to samples from populations of Costa Rican hypogean *Rhamdia* (documented herein) in red. Terminals corresponding to samples from Costa Rican epigean *Rhamdia* collected in this study in blue. Outgroup taxon (*Rhamdia quelen*) not shown. The dashed rectangle indicates the *R. guatemalensis* clade, whereas the light gray rectangle indicates the “*R. laticauda*-group” clade, inclusive of *R. nicaraguensis*, *R. parryi*, and the four Mexican stygobitic species.

living in syntopy, Gabinarraca cave in Costa Rica effectively constitutes a new model to investigate the processes allowing the local coexistence of closely related, morphologically similar, and seemingly ecologically equivalent species/populations of cavefishes. Future research aimed at generating and analyzing detailed data on diet and microhabitat occupation will be necessary to start shedding light on the ecological mechanisms allowing syntopy of *Rhamdia* catfishes in this cave system.

Given the ample taxonomic and geographic coverage, the resulting phylogenies (Figs 8–10) offer an extensive panorama of interspecific relationships within the Middle American *Rhamdia* clade and of phylogeographic structure within wide-ranging species such as *R. guatemalensis* and *R. laticauda*. As such, our phylogenetic results corroborate the relentless paraphyly of *R. laticauda* (with respect to *R. nicaraguensis*, *R. parryi*, and the Mexican stygobitic species) (Perdices et al. 2002; Arroyave and De La Cruz Fernández 2021b) and support the taxonomic distinctiveness (from *R. laticauda*) and monophyletic status of both *R. nicaraguensis* (Silfvergrip 1996; Bussing 1998) and *R. parryi* (Miller 2005), although uncertainty regarding their phylogenetic placement within the larger “*R. laticauda*-group” clade remains (Perdices et al. 2002; Arroyave and De La Cruz Fernández 2021b; Buenavad-González et al. 2023).

Phylogeographic structure in *R. guatemalensis* and *R. laticauda* appears generally consistent with a latitudinal gradient and the expectations from catchment hydrology (Perdices et al. 2002; Hernández et al. 2015; Arroyave et al. 2021). However, within these species-level clades, most internodes are short and poorly supported, rendering their phylogeographic histories unclear. The morphology-based species designations of the cave-dwelling *Rhamdia* populations reported herein were in all cases corroborated with molecular data in a phylogenetic framework (Figs 8–10). As expected from a biogeographic perspective, besides being resolved within their respective species-level clade, these hypogean populations always associated most closely with the geographically/hydrologically closest epigean populations. Samples from the Corredores cave (near the border with Panama) are more closely related to epigean populations of *R. guatemalensis* from Costa Rica and Panamá. Likewise, hypogean *Rhamdia* from Gabinarraca cave (*R. laticauda* and *R. nicaraguensis*) are more closely related—and practically genetically identical (i.e.,  $p$ -distances < 0.3%)—to epigean samples of their respective species from the same basin (Río Frío) (Figs 8–10).

This pattern, also documented for numerous cave-dwelling populations of *Rhamdia* catfishes in southern Mexico (Arroyave and De La Cruz Fernández 2021a, 2021b, Buenavad-González et al. 2023), coupled with the observed relatively incipient troglomorphy (partial depigmentation but without eye loss), suggests recent cave colonization events and/or continued gene flow between epigean and hypogean populations. Further research into this subject, ideally based on genome-wide comparative data, would be required to properly test hypotheses of gene flow and the timing of lineage divergences and cave colonizations in *Rhamdia*. Similarly, further research is needed to shed light on basic yet poorly known aspects about the ecology of cave *Rhamdia*, such as diet and demography. Although we currently lack data about their trophic ecology and population dynamics, we assume that these hypogean populations are resident, and hypothesize that their incipient troglomorphy has evolved as a result of living



**Figure 10.** Phylogenetic relationships of Middle American *Rhamdia* inferred from comparative COI + CYTB data (concatenated). Colored circles on nodes indicate degree of clade support as determined by bootstrap values: black > 95, 95 ≥ blue ≥ 75, red < 75. Terminal names as follow: Species name + GenBank accession or catalog/voucher (for new/unpublished sequences) + country, basin (in parenthesis). Terminals corresponding to samples from populations of Costa Rican hypogean *Rhamdia* (documented herein) in red. Terminals corresponding to samples from Costa Rican epigean *Rhamdia* collected in this study in blue. Outgroup taxon (*Rhamdia quelen*) not shown. The dashed rectangle indicates the *R. guatemalensis* clade, whereas the light gray rectangle indicates the “*R. laticauda*-group” clade, inclusive of *R. nicaraguensis*, *R. parryi*, and the four Mexican stygobitic species.

in subterranean environments, a hypothesis subject to future testing. The results from recent population genomics studies conducted on other cavefish complexes such as *Astyanax mexicanus* (Garduño-Sánchez et al. 2023) and *Typhlichthys subterraneus* (Hart et al. 2024) suggest that analyses of genome-wide data in a phylogeographic framework are a promising avenue for investigating modes of cave-adapted evolution in other fishes with cave-dwelling populations such as *Rhamdia*.

In conclusion, this study adds to a body of work showcasing the continued discovery of cave-dwelling populations of *Rhamdia* catfishes during targeted ichthyological surveys in karstic regions of Middle America (Arroyave and De La Cruz Fernández 2021a, Buenavad-González et al. 2023), and as such, it reinforces the notion that our understanding of the diversity of hypogean *Rhamdia* is only partial and that sustained exploration and taxonomically sound documentation work are paramount to advancing knowledge about the diversity and evolution of these group of Neotropical catfishes. We hope that by uncovering and taxonomically documenting cavefish diversity present in Costa Rica and its karstic systems, this study opens the gates for future research on the subject in the region.

## Acknowledgements

This research was financially supported by the Universidad Nacional Autónoma de México (UNAM) through a “Programa de Apoyo a Proyectos de Investigación e Innovación Tecnológica (PAPIIT)” grant (IN214922) to JA, the Vicerrectoría de Investigación de la Universidad de Costa Rica (UCR) through research projects C1125, C2763 and B6773-23 to AA, and a grant from the Walder Foundation to CDM. Special thanks to the firemen from Ciudad Neily (Benemérito Cuerpo de Bomberos de Costa Rica, Estación Ciudad Neily) who accompanied and supported us during our sampling of Corredores cave. Additional thanks to A. Jiménez-Marin, N. López, and L. Márquez (Laboratorio de Biología Molecular, LaNaBio, Instituto de Biología, UNAM), and to Diego Elías (Field Museum of Natural History) for their support during the generation of the DNA sequence data used in this study.

## References

- Arroyave J, De La Cruz Fernández DA (2021a) Cave-dwelling populations of *Rhamdia* (Siluriformes: Heptapteridae) from the Sierra de Zongolica, Veracruz, Mexico: an evidence-based checklist with comments on their evolutionary history and taxonomy. *Journal of Fish Biology* 99: 283–287. <https://doi.org/10.1111/jfb.14713>
- Arroyave J, De La Cruz Fernández DA (2021b) Genetic and morphological evidence cast doubt on the validity of Mexican troglotic species of the Neotropical catfish genus *Rhamdia* (Siluriformes: Heptapteridae). *Revista Mexicana de Biodiversidad* 92: 1–32. <https://doi.org/10.22201/ib.20078706e.2021.92.3718>

- Arroyave J, Martinez CM, Martínez-Oriol FH, Sosa E, Alter SE (2021) Regional-scale aquifer hydrogeology as a driver of phylogeographic structure in the Neotropical catfish *Rhamdia guatemalensis* (Siluriformes: Heptapteridae) from cenotes of the Yucatán Peninsula, Mexico. *Freshwater Biology* 66: 332–348. <https://doi.org/10.1111/fwb.13641>
- Avalos G (2018) Still Searching the Rich Coast: Biodiversity of Costa Rica, Numbers, Processes, Patterns, and Challenges. In: *Global Biodiversity*. Apple Academic Press, 35 pp. <https://doi.org/10.1201/9780429433634-4>
- Bichuette ME, Trajano E (2005) A new cave species of *Rhamdia* (Siluriformes: Heptapteridae) from Serra do Ramalho, northeastern Brazil, with notes on ecology and behavior. *Neotropical Ichthyology* 3: 587–595. <https://doi.org/10.1590/S1679-62252005000400016>
- Buenavad-González MA, López-Vila JM, Torres-Vázquez D, Hernández-Ávila SG, Zárate-Gálvez K, Arroyave J (2023) New records of cave-dwelling populations of *Rhamdia* catfishes (Siluriformes, Heptapteridae) from Chiapas, Mexico. *Subterranean Biology* 46: 61–76. <https://doi.org/10.3897/subtbiol.46.110269>
- Bussing WA (1998) *Freshwater fishes of Costa Rica / Peces de las aguas continentales de Costa Rica*. Editorial de la Universidad de Costa Rica, San José, Costa Rica, 496 pp.
- Ceríaco LM, Gutiérrez EE, Dubois A (2016) Photography-based taxonomy is inadequate, unnecessary, and potentially harmful for biological sciences. *Zootaxa* 4196(3): 435–445. <https://doi.org/10.11646/zootaxa.4196.3.9>
- Chesnel V, Rodríguez E (2021) Facies analysis of a Bartonian–Aquitania siliciclastic-carbonate system, Costa Rica. *Sedimentary Geology* 417: 105884. <https://doi.org/10.1016/j.sedg-geo.2021.105884>
- Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: more models, new heuristics and parallel computing. *Nature Methods* 9: 772–772. <https://doi.org/10.1038/nmeth.2109>
- Debeljak GC (1988) *Ricerche e Scoperte Speleologiche Costa Rica* 88. Trieste. Cave-dwelling fauna of Costa Rica, 57 pp.
- Deleva S, Ulloa A, Oliveira HFM, Simov N, Didonna F, Chaverri G (2023) Cave-dwelling fauna of Costa Rica: current state of knowledge and future research perspectives. *Subterranean Biology* 47: 29–62. <https://doi.org/10.3897/subtbiol.47.113219>
- DoNascimento C, Provenzano F, Lundberg JG (2004) *Rhamdia guasarensis* (Siluriformes: Heptapteridae), a new species of cave catfish from the Sierra de Perijá, northwestern Venezuela. *Proceedings of the Biological Society of Washington* 117: 564–574.
- Edgar RC (2004) MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics* 5: 113. <https://doi.org/10.1186/1471-2105-5-113>
- Felsenstein J (1981) Evolutionary trees from DNA sequences: A maximum likelihood approach. *Journal of Molecular Evolution* 17: 368–376. <https://doi.org/10.1007/BF01734359>
- Fricke R, Eschmeyer WN, Van der Laan R (2024) Eschmeyer's catalog of fishes: genera, species, references. <http://researcharchive.calacademy.org/research/ichthyology/catalog/fish-catmain.asp> [June 10, 2024]
- Garduño-Sánchez M, Hernández-Lozano J, Moran RL, Miranda-Gamboa R, Gross JB, Rohner N, Elliott WR, Miller J, Lozano-Vilano L, McGaugh SE, Ornelas-García CP (2023) Phylogeographic relationships and morphological evolution between cave and surface *Astyanax mexicanus* populations (De Filippi 1853) (Actinopterygii, Characidae). *Molecular Ecology* 32(20): 5626–5644. <https://doi.org/10.1111/mec.17128>

- Hart PB, Niemiller ML, Armbruster JW, Chakrabarty P (2024) Conservation implications for the world's most widely distributed cavefish species complex based on population genomics (*Typhlichthys*, Percopsiformes). *Conservation Genetics* 25: 165–177. <https://doi.org/10.1007/s10592-023-01562-x>
- Hernández CL, Ortega-Lara A, Sánchez-Garcés GC, Alford MH (2015) Genetic and Morphometric Evidence for the Recognition of Several Recently Synonymized Species of Trans-Andean *Rhamdia* (Pisces: Siluriformes: Heptapteridae). *Copeia* 103: 563–579. <https://doi.org/10.1643/CI-14-145>
- Hubbs CL (1938) Fishes from the caves of Yucatan. *Publications of the Carnegie Institution of Washington* 491: 261–295.
- Jenkins JA, Bart Jr HL, Bowker JD, Bowser PR, MacMillan JR, Nickum JG, Rose JD, Sorensen PW, Whitedge GW, Rachlin JW (2014) Guidelines for the Use of Fishes in Research. Bethesda, Maryland, USA: American Fisheries Society, 104 pp. <https://doi.org/10.47886/9781934874394>
- Juberthie C, Strinati P (1994) *Encyclopedie Biospeologique*. Tome I, Cap. IV. Historique de la Biospologie 1.
- Kozlov AM, Darriba D, Flouri T, Morel B, Stamatakis A (2019) RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. *Bioinformatics* 35: 4453–4455. <https://doi.org/10.1093/bioinformatics/btz305>
- Miller RR (1984) *Rhamdia reddelli* new species, the first blind pimelodid catfish from Middle America, with a key to the Mexican species. *Transactions of the San Diego Society of Natural History* 20(8): 135–144. <https://doi.org/10.5962/bhl.part.29002>
- Miller RR (2005) Freshwater fishes of Mexico (with the collaboration of WL Minkley and SM Norris). The University of Chicago Press, Chicago, IL, 652 pp.
- Nachman MW, Beckman EJ, Bowie RC, Cicero C, Conroy CJ, Dudley R, Hayes TB, Koo MS, Lacey EA, Martin CH, McGuire JA, Patton JL, Spencer CL, Tarvin RD, Wake MH, Wang IJ, Achmadi A, Álvarez-Castañeda ST, Andersen MJ, Arroyave J, Austin CC, Barker FK, Barrow LN, Barrowclough GF, Bates J, Bauer AM, Bell KC, Bell RC, Bronson AW, Brown RM, Burbrink FT, Burns KJ, Cadena CD, Cannatella DC, Castoe TA, Chakrabarty P, Colella JP, Cook JA, Cracraft JL, Davis DR, Davis Rabosky AR, D'Elia G, Dumbacher JP, Dunnum JL, Edwards SV, Esselstyn JA, Faivovich J, Fjeldså J, Flores-Villela OA, Ford K, Fuchs J, Fujita MK, Good JM, Greenbaum E, Greene HW, Hackett S, Hamidy A, Hanken J, Haryoko T, Hawkins MT, Heaney LR, Hillis DM, Hollingsworth BD, Hornsby AD, Hosner PA, Irham M, Jansa S, Jiménez RA, Joseph L, Kirchman JJ, LaDuc TJ, Leaché AD, Lessa EP, López-Fernández H, Mason NA, McCormack JE, McMahan CD, Moyle RG, Ojeda RA, Olson LE, Kin Onn C, Parenti LR, Parra-Olea G, Patterson BD, Pauly GB, Pavan SE, Peterson AT, Poe S, Rabosky DL, Raxworthy CJ, Reddy S, Rico-Guevara A, Riyanto A, Rocha LA, Ron SR, Rovito SM, Rowe KC, Rowley J, Ruane S, Salazar-Valenzuela D, Shultz AJ, Sidlauskas B, Sikes DS, Simmons NB, Stiasny MLJ, Streicher JW, Stuart BL, Summers AP, Tavera J, Teta P, Thompson CW, Timm RM, Torres-Carvajal O, Voelker G, Voss RS, Winker K, Witt C, Wommack EA, Zink RM (2023) Specimen collection is essential for modern science. *PLoS Biology* 21(11): e3002318. <https://doi.org/10.1371/journal.pbio.3002318>
- Niemiller ML, Soares D (2015) Cave Environments. In: Riesch R, Tobler M, Plath M (Eds) *Extremophile Fishes: Ecology, Evolution, and Physiology of Teleosts in Extreme*

- Environments. Springer International Publishing, Cham, 161–191. [https://doi.org/10.1007/978-3-319-13362-1\\_8](https://doi.org/10.1007/978-3-319-13362-1_8)
- Peacock N, Hempel J (1993) Studies in the Rio Corredor basin. The NSS Bulletin. Journal of Caves and Karst Studies 55: 134–134.
- Perdices A, Bermingham E, Montilla A, Doadrio I (2002) Evolutionary history of the genus *Rhamdia* (Teleostei: Pimelodidae) in Central America. Molecular Phylogenetics and Evolution 25: 172–189. [https://doi.org/10.1016/S1055-7903\(02\)00224-5](https://doi.org/10.1016/S1055-7903(02)00224-5)
- Pianka ER (1973) The Structure of Lizard Communities. Annual Review of Ecology and Systematics 4: 53–74. <https://doi.org/10.1146/annurev.es.04.110173.000413>
- Rocha LA, Aleixo A, Allen G, Almeda F, Baldwin CC, Barclay VLM, Bates JM, Bauer AM, Benzoni F, Berns CM, Berumen ML, Blackburn DC, Blum S, Bolaños F, Bowie RCK, Britz R, Brown RM, Cadena CD, Carpenter K, Ceríaco P, Chakrabarty LM, Chaves G, Choat JH, Clements KD, Collette BB, Collins A, Coyne J, Cracraft J, Daniel T, De Carvalho MR, De Queiroz K et al. (2014) Specimen collection: An essential tool. Science 344(6186): 814–815. <https://doi.org/10.1126/science.344.6186.814>
- Salinas NR, Little DP (2014) 2matrix: A utility for indel coding and phylogenetic matrix concatenation1. Applications in Plant Sciences 2(1): 1300083. <https://doi.org/10.3732/apps.1300083>
- Sandí XG (2012) Murciélagos en refugios artificiales: Diversidad de murciélagos y caracterización de factores ambientales en un túnel, Guanacaste, Costa Rica. Editorial Académica Española, 84 pp.
- Silfvergrip AMC (1996) A systematic revision of the Neotropical catfish genus *Rhamdia* (Teleostei, Pimelodidae). Stockholm University, 156 pp.
- Strinati P, Goicoechea C, Cortés G (1987) Quelques grottes du Costa Rica et leur faune. Actes du 8: 23–32.
- Trajano E (2001) Ecology of Subterranean Fishes: An Overview. Environmental Biology of Fishes 62: 133–160. <https://doi.org/10.1023/A:1011841913569>
- Ulloa A, Aguilar T, Goicoechea C, Ramírez R (2011) Descripción, clasificación y aspectos geológicos de las zonas kársticas de Costa Rica. Revista Geológica de América Central 45: 53–74.
- Ulloa A, Argüello A, Obando A, Vargas M, Ulloa A, Argüello A, Obando A, Vargas M (2021) Geomorfología y espeleogénesis del sistema kárstico de Cuevas de Venado, Costa Rica. Revista Geológica de América Central: 58–89. <https://doi.org/10.15517/rgac.v0i64.46619>
- Weber A, Wilkens H (1998) *Rhamdia macuspanensis*: A New Species of Troglotic Pimelodid Catfish (Siluriformes; Pimelodidae) from a Cave in Tabasco, Mexico. Copeia 1998: 998–1004. <https://doi.org/10.2307/1447347>
- Weber A, Allegrucci G, Sbordoni V (2003) *Rhamdia laluchensis*, a new species of troglotic catfish (Siluriformes: Pimelodidae) from Chiapas, Mexico. Ichthyological Exploration of Freshwaters 14: 273–280.
- Wilkens H (1993) A new species of *Rhamdia* (Pisces: Pimelodidae) from a cave in the Sierra de Zongolica (Veracruz, México). Mitteilungen aus dem Hamburgischen Zoologischen Museum und Institut 90: 375–378.